

Single Cell Mouse Hematopoietic Stem and Progenitor Cell Differentiation

Group: Kevin Benac, Boying Gong, George Shan, and Tae Won Chung

Diffusion Map

```
library(destiny)
# library(plot3D)
library(dynamicTreeCut)
library(RColorBrewer)
library(slingshot)

## Loading required package: Biobase

## Loading required package: BiocGenerics

## Loading required package: methods

## Loading required package: parallel

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
##
##   clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##   clusterExport, clusterMap, parApply, parCapply, parLapply,
##   parLapplyLB, parRapply, parSapply, parSapplyLB

## The following objects are masked from 'package:stats':
##
##   IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, cbind, colMeans,
##   colnames, colSums, do.call, duplicated, eval, evalq, Filter,
##   Find, get, grep, grepl, intersect, is.unsorted, lapply,
##   lengths, Map, mapply, match, mget, order, paste, pmax,
##   pmax.int, pmin, pmin.int, Position, rank, rbind, Reduce,
##   rowMeans, rownames, rowSums, sapply, setdiff, sort, table,
##   tapply, union, unique, unsplit, which, which.max, which.min

## Welcome to Bioconductor
##
##   Vignettes contain introductory material; view with
##   'browseVignettes()'. To cite Bioconductor, see
##   'citation("Biobase")', and for packages 'citation("pkgname")'.
```

```
## Loading required package: prncurve
```

```
data <- as.matrix(read.table("data/normalisedCountsVariableGenes.txt", header=TRUE, sep = ""))  
dim(data) # Verify this is 4773 by 1656
```

```
## [1] 4773 1656
```

```
data_log <- log2(data+1)
```

```
# Part 1.
```

```
dist_spearman <- as.dist((1-cor(data, method="spearman"))/2)
```

```
clusters<-hclust(d=dist_spearman, method="average")
```

```
clusters_discrete<-cutreeDynamic(clusters, method="hybrid", distM=as.matrix(dist_spearman), minClusterS
```

```
## ..cutHeight not given, setting it to 0.3 ==> 99% of the (truncated) height range in dendro.
```

```
## ..done.
```

```
# Part 2.
```

```
diffmap <- DiffusionMap(data=t(data_log), sigma=0.16, distance = "cosine") # This will take some time
```

```
# scatter3D(x=diffmap$DC3, y=diffmap$DC1, z=diffmap$DC2, theta = -110, phi=20, xlab="DC3", ylab="DC1",
```

```
# colvar=as.numeric(clusters_discrete), col=c("black","purple","magenta","cyan","yellow","blue")
```

Pseudotimes

Notice that there are only two unclustered (cluster=0), so we ignore the third #lineage. Lineage 1 is the lineage for differentiation into white blood cells. Lineage 2 is the lineage for differentiation into red blood cells and Megakaryocytes. Megakaryocytes are rare, so most of lineage 2 is probably pre-erythrocyte (rbc). RBC's are weird in that they lack nuclei and are basically carriers for hemoglobin, #which means that alot of significant gene expression had to have occurred to cause this #cell fate. This is consistent with seeing how DC1 is basically defined by cluster 2 #being apart from the others

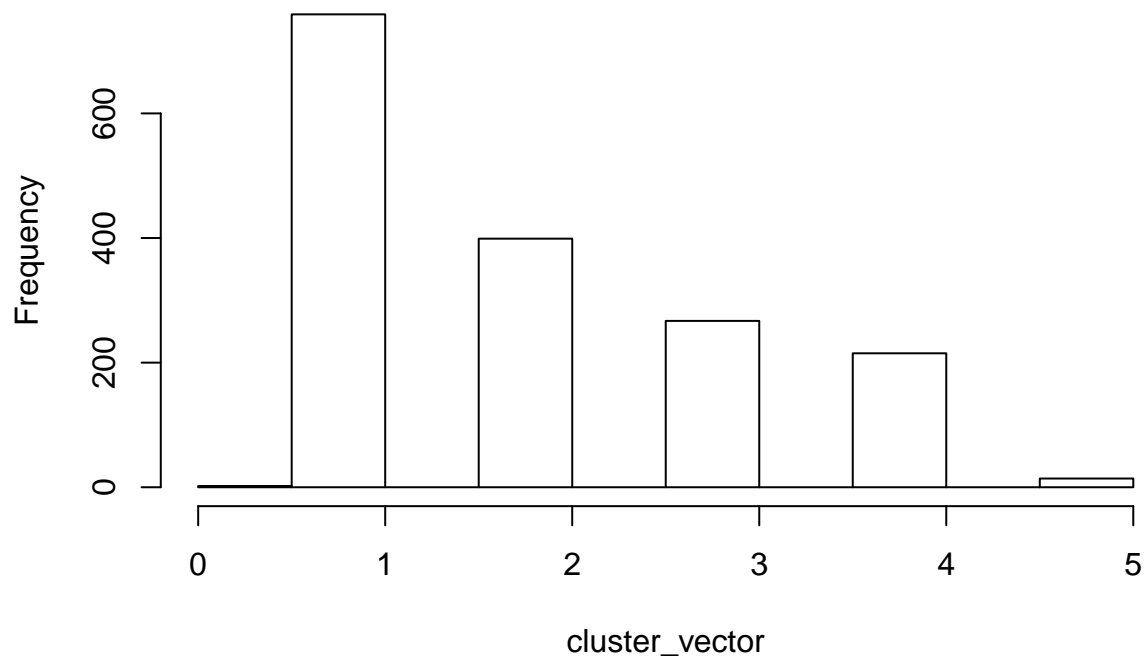
```
cluster_vector<-as.vector(clusters_discrete)
```

```
which(cluster_vector==0)
```

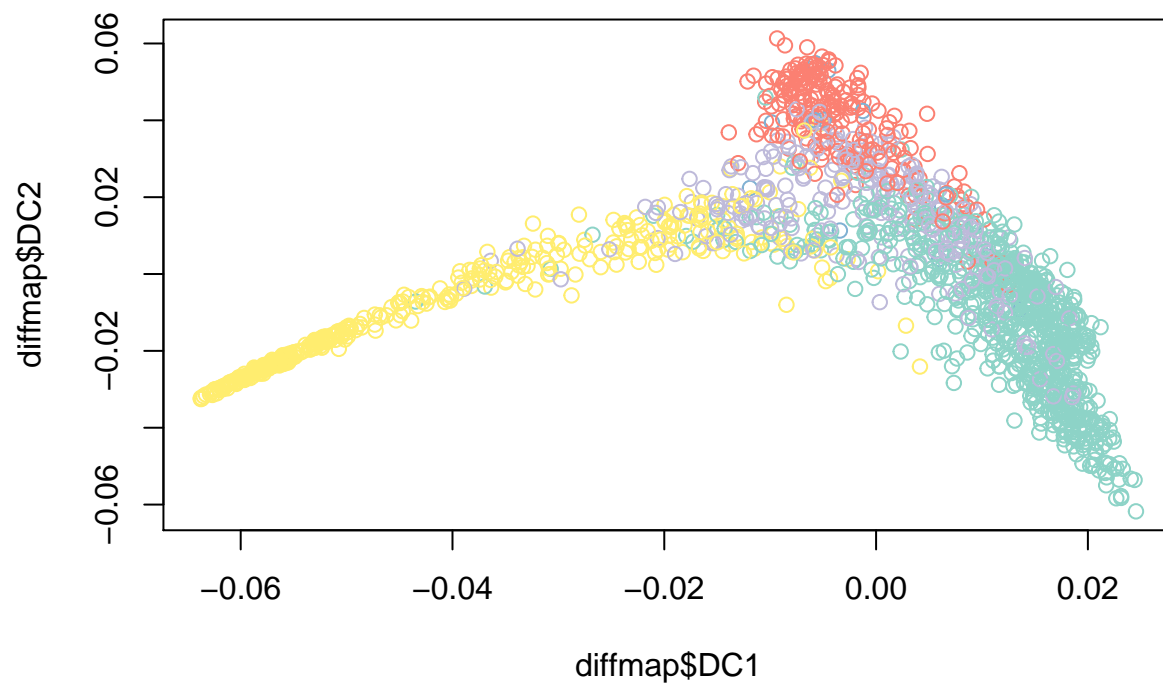
```
## [1] 1096 1115
```

```
hist(cluster_vector)
```

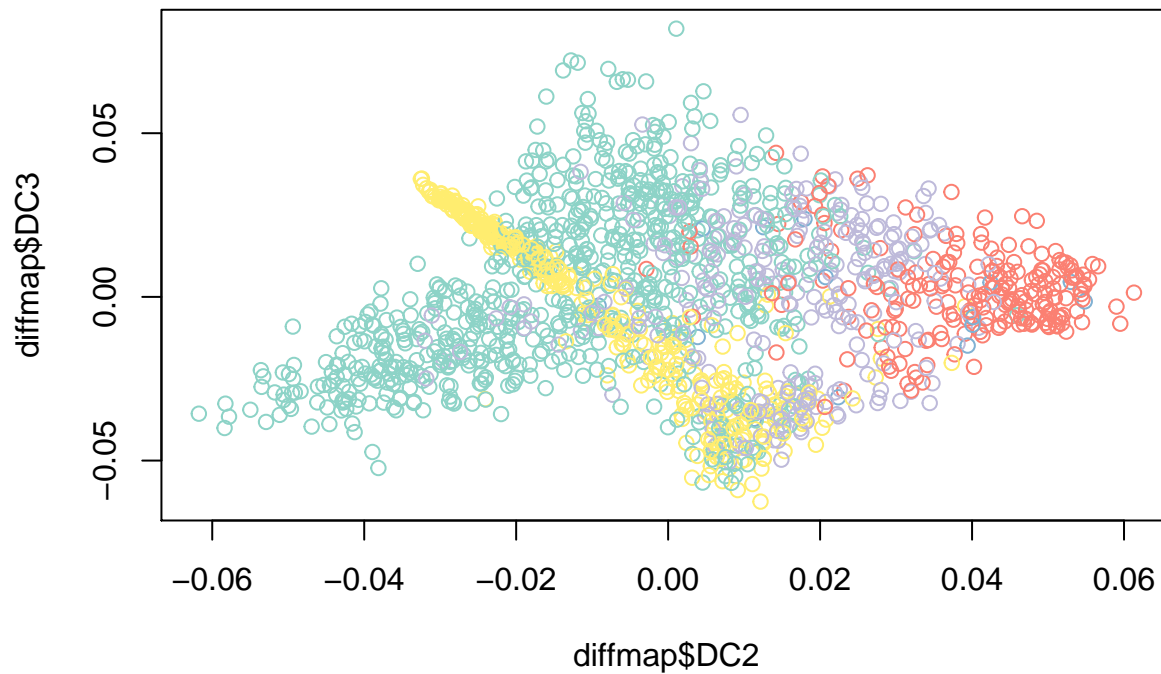
Histogram of cluster_vector



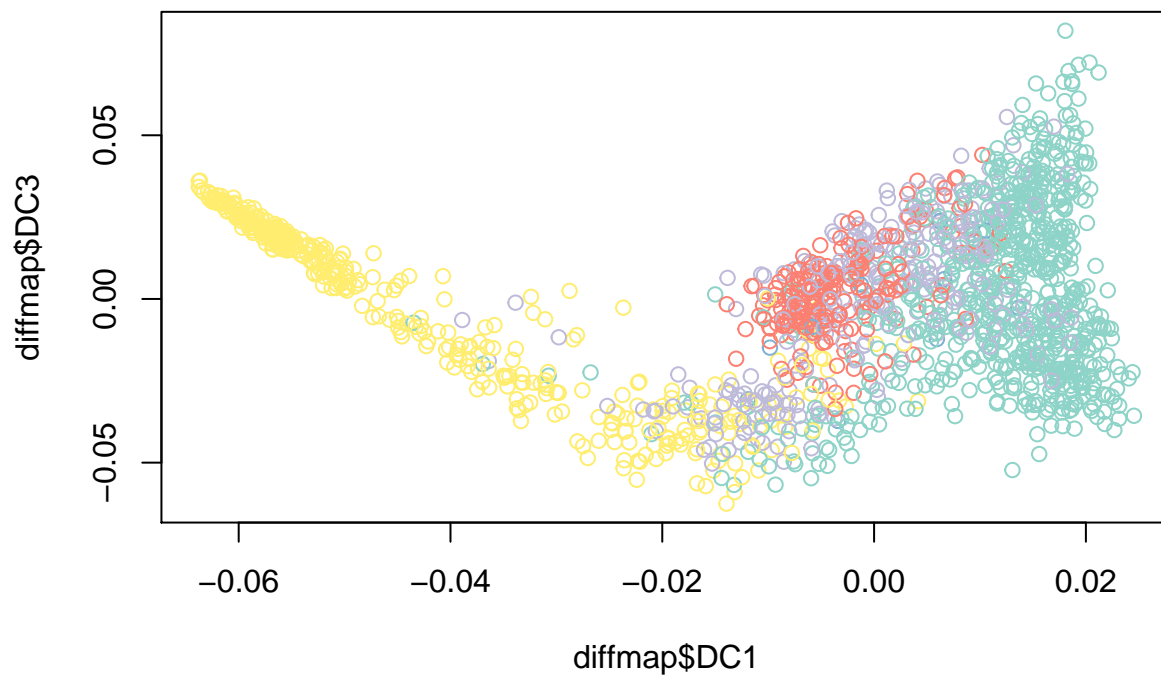
```
rd<-cbind(diffmap$DC1, diffmap$DC2, diffmap$DC3)
plot(diffmap$DC1,diffmap$DC2, col=cluster_vector)
```



```
plot(diffmap$DC2,diffmap$DC3, col=cluster_vector)
```



```
plot(diffmap$DC1,diffmap$DC3, col=cluster_vector)
```



```
sds<-slingshot(rd, cluster_vector, start.clus=1)
```

```
## Using diagonal covariance matrix
```

```
sds
```

```
## class: SlingshotDataSet
```

```
##
## Samples Dimensions
##      1656      3
##
## lineages: 3
## Lineage1: 1  3  5  4
## Lineage2: 1  3  2
## Lineage3: 1  0
##
## curves: 3
## Curve1: Length: 0.13876 Samples: 822.87
## Curve2: Length: 0.20971 Samples: 976.34
## Curve3: Length: 0.13603 Samples: 609.92
```

```
psdt<-pseudotime(sds)
```

```
head(cbind(psdt,cluster_vector), 100)
```

##	curve1	curve2	curve3	cluster_vector
## Cell-1	0.04765777	0.04775829	NA	3
## Cell-2	0.05351497	0.05113183	0.05211391	1
## Cell-3	0.03223960	0.03221008	0.03233601	1
## Cell-4	0.06623187	0.06150331	0.10255115	1
## Cell-5	0.06792297	0.06549150	0.09061651	1
## Cell-6	0.05887061	0.05444123	0.05662301	1
## Cell-7	0.04382467	0.04159929	0.04297008	1
## Cell-8	0.07225748	0.07982840	0.12206336	1
## Cell-9	0.03153914	0.03164424	NA	3
## Cell-10	0.00000000	0.00000000	0.00000000	1
## Cell-11	0.06200211	0.05944892	0.06159530	1
## Cell-12	0.07125159	0.07198024	0.08855529	1
## Cell-13	0.03881832	0.03966941	0.03867846	1
## Cell-14	0.04384412	0.04181709	0.04305120	1
## Cell-15	0.07649336	0.07308640	0.07105777	1
## Cell-16	0.10057401	0.05406095	NA	3
## Cell-17	0.02139675	0.02143292	0.02150561	1
## Cell-18	0.07919309	0.08258857	0.07509610	1
## Cell-19	0.11285760	NA	NA	4
## Cell-20	0.03125630	0.03129743	0.03087749	1
## Cell-21	0.08276955	0.08900068	NA	3
## Cell-22	0.03083715	0.03083437	NA	3
## Cell-23	0.11279331	0.06490648	NA	3
## Cell-24	0.02643334	0.02646441	0.02656401	1
## Cell-25	0.07085666	NA	0.10479988	1
## Cell-26	0.03887090	0.03874093	0.03881154	1
## Cell-27	0.01792333	0.01789727	NA	3
## Cell-28	0.06741237	0.06433865	0.09659694	1
## Cell-29	0.03395041	0.03390828	0.03397351	1
## Cell-30	0.06791750	0.06555054	0.08724415	1
## Cell-31	0.03868308	0.03826946	0.03866266	1
## Cell-32	0.03681710	0.03743749	0.03652017	1
## Cell-33	0.05922492	0.05864560	0.05910310	1
## Cell-34	0.05712099	0.05204938	0.05415246	1
## Cell-35	0.01087548	0.01087170	0.01086525	1

## Cell-36	0.10950309	0.06068250	NA	3
## Cell-37	0.02588606	0.02587065	0.02582458	1
## Cell-38	0.04493061	0.04368059	0.04437288	1
## Cell-39	0.03059680	0.03063040	NA	3
## Cell-40	0.13876126	NA	NA	4
## Cell-41	0.10189277	NA	NA	4
## Cell-42	0.12823001	NA	NA	4
## Cell-43	NA	0.17935945	NA	2
## Cell-44	0.08689648	0.08497288	0.07165452	1
## Cell-45	NA	0.11683090	NA	2
## Cell-46	0.13370967	NA	NA	4
## Cell-47	NA	0.20615673	NA	2
## Cell-48	NA	0.18952304	NA	2
## Cell-49	NA	0.14773131	NA	2
## Cell-50	0.09654595	0.06342065	NA	3
## Cell-51	NA	0.18741014	NA	2
## Cell-52	NA	0.16963732	NA	2
## Cell-53	NA	0.13812580	NA	2
## Cell-54	NA	0.18714437	NA	2
## Cell-55	0.11255758	0.03983579	NA	3
## Cell-56	NA	0.18845858	NA	2
## Cell-57	NA	0.09849427	NA	2
## Cell-58	NA	0.18597380	NA	2
## Cell-59	NA	0.20097275	NA	2
## Cell-60	0.07020584	NA	0.10254237	1
## Cell-61	NA	0.12892613	NA	2
## Cell-62	0.10097316	0.07981943	NA	3
## Cell-63	NA	0.18111143	NA	2
## Cell-64	NA	0.18661763	NA	2
## Cell-65	NA	0.14395494	NA	2
## Cell-66	0.05654897	0.05680090	0.05678926	1
## Cell-67	0.11413799	0.04375791	NA	3
## Cell-68	NA	0.10944691	NA	2
## Cell-69	NA	0.17679361	NA	2
## Cell-70	0.13287095	NA	NA	4
## Cell-71	NA	0.10637407	NA	2
## Cell-72	NA	0.20247441	NA	2
## Cell-73	NA	0.18875428	NA	2
## Cell-74	0.07098004	NA	0.10599399	1
## Cell-75	0.09805135	0.06450495	NA	3
## Cell-76	NA	0.19737547	NA	2
## Cell-77	NA	0.12378200	NA	2
## Cell-78	NA	0.11366224	NA	2
## Cell-79	NA	0.15403668	NA	2
## Cell-80	NA	0.14767172	NA	2
## Cell-81	NA	0.20700646	NA	2
## Cell-82	0.04218191	0.04221289	0.04211215	1
## Cell-83	0.09611015	0.06513640	NA	3
## Cell-84	0.04503997	0.04630934	NA	3
## Cell-85	0.04576554	0.04607272	0.04581396	1
## Cell-86	0.04405785	0.04411617	0.04400366	1
## Cell-87	0.09062525	0.07795360	0.06782521	1
## Cell-88	0.06858132	NA	0.10172909	1
## Cell-89	0.04673783	0.04819490	0.04732474	1

## Cell-90	0.03232529	0.03249416	NA	3
## Cell-91	0.03703299	0.03714553	0.03692169	1
## Cell-92	0.08306471	0.08641024	NA	3
## Cell-93	0.04029330	0.04088864	0.04027378	1
## Cell-94	0.07110473	0.07204589	0.09149883	1
## Cell-95	0.03931608	0.03975525	0.03922018	1
## Cell-96	0.06699586	0.06287899	0.10490671	1
## Cell-97	0.13031735	NA	NA	4
## Cell-98	0.03230470	0.03218475	0.03267832	1
## Cell-99	0.07220254	0.07807610	0.11426088	1
## Cell-100	0.13452037	NA	NA	4

```
save(psd, cluster_vector, file="output/pseudotimes.RData")
```